

SEQUENCE LISTING

<110> Lowery, David E.
Smith, Valdin G.
Kubiak, Teresa M.
Larsen, Martha J.

<120> Drosophila G Protein Coupled Receptors, Nucleic Acids, and
Methods Related to the Same

<130> PHRM0002-105

<140> US 10/523,893
<141> 2005-02-04

<150> US 10/283,423
<151> 2002-10-30

<150> US 09/693,746
<151> 2000-10-20

<150> US 09/425,676
<151> 1999-10-22

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<170> PatentIn version 3.3

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Thr	Ser	Pro	Gly	Thr	Thr	Ser	Ala	Ile	Leu	Ala	Asp	Val	Ala	Ala	Ser
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Phe Phe Tyr Val Leu Tyr Ala Thr Val Phe Val Leu Gly Val Phe Gly
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Asn Val Leu Val Cys Tyr Val Val Leu Arg Asn Arg Ala Met Gln Thr
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Cys Val Leu Ala Val Pro Phe Thr Pro Leu Tyr Thr Phe Met Gly Arg
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Cys Ser Ile Tyr Ile Ser Thr Leu Thr Leu Thr Ser Ile Ala Ile Asp
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Arg Tyr Phe Val Ile Ile Tyr Pro Phe His Pro Arg Met Lys Leu Ser
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Thr Cys Ile Gly Ile Ile Val Ser Ile Trp Val Ile Ala Leu Leu Ala
180 185 190

Thr Val Pro Tyr Gly Met Tyr Met Lys Met Thr Asn Glu Leu Val Asn
195 200 205

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Thr Gly Pro Glu Met Pro Tyr Val Arg Val Tyr Cys Glu Glu Asn Trp
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Pro Ser Glu Gln Tyr Arg Lys Val Phe Gly Ala Ile Thr Thr Thr Leu
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Arg Lys Glu Phe Lys His Val Leu Pro Cys Phe Asn Pro Ser Asn Asn
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Cys Gly Pro Arg Leu His His Gly Lys Gly Asp Gly Gly Met Gly Gly
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Gly Ser Leu Asp Ala Asp Asp Gln Asp Glu Asn Gly Ile Thr Gln Glu
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Thr Cys Leu Pro Lys Glu Lys Leu Leu Ile Ile Pro Arg Glu Pro Thr
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Tyr Gly Asn Gly Thr Gly Ala Val Ser Pro Ile Leu Ser Gly Arg Gly
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Ile Asn Ala Ala Leu Val His Gly Gly Asp His Gln Met His Gln Leu
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Gln Pro Ser His His Gln Gln Val Glu Leu Thr Arg Arg Ile Arg Arg
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Thr Thr Gly Ile Ser Ile Leu Glu Thr Ser Thr Ser His Cys Gln Asp
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Ala Glu Leu Gly Arg Arg Ile Asn
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Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
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Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val
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Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
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His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
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Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
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Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
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Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
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Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
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Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
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Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
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Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe
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Ser Thr Thr Gly Leu
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Ala Ile Asn Thr Ser Asp Leu Asn Glu Thr Gly Ser Arg Pro Leu Asp
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Pro Val Leu Ile Asp Arg Phe Leu Ser Asn Arg Ala Val Asp Ser Pro
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Trp Tyr His Met Leu Ile Ser Met Tyr Gly Val Leu Ile Val Phe Gly
85 90 95

Ala Leu Gly Asn Thr Leu Val Val Ile Ala Val Ile Arg Lys Pro Ile
100 105 110

Met Arg Thr Ala Arg Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp
115 120 125

Leu Leu Leu Cys Leu Val Thr Met Pro Leu Thr Leu Met Glu Ile Leu
130 135 140

Ser Lys Tyr Trp Pro Tyr Gly Ser Cys Ser Ile Leu Cys Lys Thr Ile
145 150 155 160

Ala Met Leu Gln Ala Leu Cys Ile Phe Val Ser Thr Ile Ser Ile Thr

165 170 175

Ala Ile Ala Phe Asp Arg Tyr Gln Val Ile Val Tyr Pro Thr Arg Asp
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195 200 205

Leu Ala Leu Leu Ala Ser Pro Leu Phe Val Tyr Lys Glu Leu Ile
210 215 220

Asn Thr Asp Thr Pro Ala Leu Leu Gln Gln Ile Gly Leu Gln Asp Thr
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Ile Pro Tyr Cys Ile Glu Asp Trp Pro Ser Arg Asn Gly Arg Phe Tyr
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Tyr Ser Ile Phe Ser Leu Cys Val Gln Tyr Leu Val Pro Ile Leu Ile
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Val Ser Val Ala Tyr Phe Gly Ile Tyr Asn Lys Leu Lys Ser Arg Ile
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Thr Val Val Ala Val Gln Ala Ser Ser Ala Gln Arg Lys Val Glu Arg
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Gly Arg Arg Met Lys Arg Thr Asn Cys Leu Leu Ile Ser Ile Ala Ile
305 310 315 320

Ile Phe Gly Val Ser Trp Leu Pro Leu Asn Phe Phe Asn Leu Tyr Ala
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Asp Met Glu Arg Ser Pro Val Thr Gln Ser Met Leu Val Arg Tyr Ala
340 345 350

Ile Cys His Met Ile Gly Met Ser Ser Ala Cys Ser Asn Pro Leu Leu
355 360 365

Tyr Gly Trp Leu Asn Asp Asn Phe Arg Cys Asn Val Gln Ala Ala Ala
370 375 380

Arg Lys Arg Arg Lys Leu Gly Ala Glu Leu Ser Lys Gly Glu Leu Lys
385 390 395 400

Leu Leu Gly Pro Gly Gly Ala Gln Ser Gly Thr Ala Gly Gly Glu Gly
405 410 415

Gly Leu Ala Ala Thr Asp Phe Met Thr Gly His His Glu Gly Gly Leu
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Arg Ser Ala Ile Thr Glu Ser Val Ala Leu Thr Asp His Asn Pro Val
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Pro Ser Glu Val Thr Lys Leu Met Pro Arg
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1073

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Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val
50 55 60

Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu
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Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Pro Phe Thr Ala
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Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg
100 105 110

Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
115 120 125

Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile
130 135 140

Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val
145 150 155 160

Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
165 170 175

His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
180 185 190

Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
195 200 205

Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
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Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
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Leu Val Val Val Val Val Ile Ala Phe Ala Ser Leu Trp Leu Pro Val
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Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
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Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
290 295 300

Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe
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Ser Thr Thr Gly Leu
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gcgacgctgc	ggaacagtct	gccggcggag	tcactgtcgt	ccggcggatc	tggtggtgga	1440
gggcacagga	aacggttgtc	ctaccagcag	gaaatgcagc	agcgttggtc	aggacccaaat	1500
agtgccaccg	cagtgaccaa	ttccagcagt	acggccaaca	ccacccaact	gctctccctg	1559

<210> 10
 <211> 519
 <212> PRT
 <213> D. melanogaster

<400> 10

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Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val Leu Phe Ser
20 25 30

Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro Leu Pro Asp
35 40 45

Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn His Ser Gln
50 55 60

Thr Leu Ser Thr Asp Gln Pro Ala Val Gly Asp Val Glu Asp Ala Ala
65 70 75 80

Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala Phe Val Val
85 90 95

Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly Gly Met Val
100 105 110

Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile Val Met Thr
115 120 125

Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ser
130 135 140

Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe Asn Tyr Tyr
145 150 155 160

Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr Cys Lys Leu
165 170 175

Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val Phe Thr Leu
180 185 190

Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg Pro Leu Gln
195 200 205

Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala Val Ile Trp
210 215 220

Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile Tyr Arg Thr
225 230 235 240

Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val Cys Tyr Pro
245 250 255

Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu Ser Leu Tyr
260 265 270

Asn Ile Leu Ile Ile Leu Thr Tyr Phe Leu Pro Ile Val Ser Met
275 280 285

Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly Ser Lys Thr
290 295 300

Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg Ser Lys Arg
305 310 315 320

Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe Ala Ile Cys
325 330 335

Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys Tyr Pro Ala
340 345 350

Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala Ile Tyr Trp
355 360 365

Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr Cys Trp Met
370 375 380

Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg Trp Cys Leu
385 390 395 400

Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu Asn Leu Thr
405 410 415

Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg Ile Lys Arg
420 425 430

Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser Ser Pro Lys
435 440 445

Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala Thr Leu Arg
450 455 460

Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser Gly Gly Gly
465 470 475 480

Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln Gln Arg Trp
485 490 495

Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser Ser Thr Ala
500 505 510

Asn Thr Thr Gln Leu Leu Ser
515

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<211> 1568
<212> DNA
<213> D. melanogaster

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	ctctcggcca gcaaccatac gcctctgccg gactttggcc aggagctcgc cctatccacc	180
	agctccttca atcacagcca gaccctatcc accgacctgc ccgccgtcgg ggacgtggaa	240
	gacgcggccg aggatgcggc ggcgtccatg gagacgggct cgtttgcatt tgtggtcccc	300
	tggtggcgtc aggtgctctg gagcatcctc ttccggcggca tggtcattgt ggcgacggc	360
	ggtaacctga ttgttgcttg gatcgtgatg acgaccaagc ggatgcggac ggttaaccaac	420
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	aactactact acatgcttgg tagcgactgg cccttcggcg agttctactg caagttgtcc	540
	cagttcatcg cgatgctaag catctgcgcc tcagtgtca ccctaattggc catctccatc	600
	gacagatacg tggccatcat ccggccactg cagccgcggta tgagcaagcg gtgcaacctg	660
	gccatcgccg cggcatctg gctggcctcc acgctcatct cctgccccat gatgatcatc	720
	taccgcacgg aggagggtgcc ggtccgcggg ctcagcaacc gcacggctcg ctaccggag	780
	tggcccgatg ggcccaccaa tcactccacg atggagtcgg tctacaacat cctcatcatc	840
	attctaacct acttcctgcc catcgctcc atgacggtca cctactcgcg cgtggcattc	900
	gagctctggg gatccaagac catcgccgag tgcacgcccc gccaggtgga gaatgtgcgg	960
	agtaagcgaa gggtggtgaa gatgatgatt gtggtcgtcc tgatattcgc catctgctgg	1020
	ctggccgttcc acagctactt cataatcaca tcctgctacc cggccatcac ggaggcgccc	1080

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ctctcctg 1568

<210> 12
<211> 522
<212> PRT
<213> D. melanogaster

<400> 12

Met Glu Asn Arg Ser Asp Phe Glu Ala Asp Asp Tyr Gly Asp Ile Ser
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Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val
20 25 30

Leu Phe Ser Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro
35 40 45

Leu Pro Asp Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn
50 55 60

His Ser Gln Thr Leu Ser Thr Asp Leu Pro Ala Val Gly Asp Val Glu
65 70 75 80

Asp Ala Ala Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala
85 90 95

Phe Val Val Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly
100 105 110

Gly Met Val Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile
115 120 125

Val Met Thr Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val
130 135 140

Asn Leu Ser Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe
145 150 155 160

Asn Tyr Tyr Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr
165 170 175

Cys Lys Leu Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val
180 185 190

Phe Thr Leu Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg
195 200 205

Pro Leu Gln Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala
210 215 220

Val Ile Trp Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile
225 230 235 240

Tyr Arg Thr Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val
245 250 255

Cys Tyr Pro Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu
260 265 270

Ser Leu Tyr Asn Ile Leu Ile Ile Leu Thr Tyr Phe Leu Pro Ile
275 280 285

Val Ser Met Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly
290 295 300

Ser Lys Thr Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg
305 310 315 320

Ser Lys Arg Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe
325 330 335

Ala Ile Cys Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys
340 345 350

Tyr Pro Ala Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala
355 360 365

Ile Tyr Trp Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr
370 375 380

Cys Trp Met Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg
385 390 395 400

Trp Cys Leu Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu
405 410 415

Asn Leu Thr Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg
420 425 430

Ile Lys Arg Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser
435 440 445

Ser Pro Lys Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala
450 455 460

Thr Leu Arg Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser
465 470 475 480

Gly Gly Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln
485 490 495

Gln Arg Trp Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser
500 505 510

Ser Thr Ala Asn Thr Thr Gln Leu Leu Ser
515 520

<210> 13

<211> 1394

<212> DNA

<213> D. melanogaster

<400> 13

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ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaagggtcc 180

aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatac
actgtgatga tgaactttag ctgtgacgac tatgacacctc tatcgaggaa catgtggct
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aattacttta tagccagctt ggccatcggc gacatcctga tgtccttctt ctgcgttccg
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<210> 14
<211> 464
<212> PRT
<213> D. melanogaster

<400> 14

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met
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Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn
20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
50 55 60

Gly Ser Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr
 260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
290 . . . 295 . . . 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Val Ile Val Phe
 325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp
 340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
405 410 415

Met Asn Ala Thr Ser Gly Thr Gly Pro Ala Leu Pro Leu Asn Arg Met
420 425 430

Asn Thr Ser Thr Thr Tyr Ile Ser Ala Arg Arg Lys Pro Arg Ala Thr
435 440 445

Ser Leu Arg Ala Asn Pro Leu Ser Cys Gly Glu Thr Ser Pro Leu Arg
450 455 460

<210> 15

<211> 1556

<212> DNA

<212> DRAF

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ccggaccctg	catccttact	ttacaatacc	accgcactgc	cagcggacga	tgaagggtcc	180
aactatggat	atggctccac	cacaacgctc	agtggcctcc	agttcgagac	ctataatatc	240
actgtgatga	tgaactttag	ctgtgacgac	tatgacccctc	tatcgagga	catgtggtct	300
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atcgctctg	gactcgacat	ccaatgtcg	ccgtggcaca	cgaatgcga	gaaatacatt	780
tgcgcgaaa	tgtggccgtc	gcggacgcag	gagtaactact	acaccctgfc	cctctcgcg	840
ctgcagttcg	tcgtgccgct	gggcgtgctc	atcttacact	acgcccggat	caccattcgc	900
gtctggcga	aacgaccgccc	aggcgaggcg	gaaaccaacc	gcgaccagcg	gatggcacgc	960
tccaaacgga	agatggtcaa	aatgatgctg	acggttgtga	ttgtgttcac	ctgctgttgg	1020
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<210> 16

<211> 518

<212> PRT

<213> D. Melanogaster

<400> 16

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met
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Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn
20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile

210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr
260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Asn Asp
340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
405 410 415

Met Asn Ala Thr Ser Gly Glu Met Thr Thr Lys Tyr His Arg His Val
420 425 430

Gly Asp Ala Leu Phe Arg Lys Pro Lys Ile Cys Ile Arg Asn Gly Ser
435 440 445

Ser Thr Ser Ser Gln Ser Asn Glu His Ile His His Leu His Gln Arg
450 455 460

Ser Ser Lys Ala Thr Ser Asp Ile Phe Ala Ser Glu Pro Ile Ile Met
465 470 475 480

Arg Arg Asp Val Thr Thr Ala Val Ala Val Ile Ser Lys Asn Lys Thr
485 490 495

Asp Ser Pro Val Arg Arg Ser Gly Ser Ser Gly Gly Thr Glu Ala Asn
500 505 510

Ile Arg Ser Thr Glu Phe
515

<210> 17
<211> 1628
<212> DNA
<213> D. melanogaster

<400> 17
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ttctatgggg gaatcagttat cgtggccgtc attggcaaca ctgggtcat ctgggtggtg 120
gccacgacca ggcaaattgcg gaccgtgaca aatatgtata tcgctaattt ggctttgcc 180
gatgtgatta ttggcctctt ctgcatacca tttcagttcc aggctgccct gctgcagagt
tggaacctgc cgtggttcat gtgcagcttc tgcccttcg tccaggccct gagtgtaaat 240
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gccctgctat ttgcggtgcc ctttgccatt gccttcgtg tggaggagtt gaccgaaaga 420
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aatattctgt atgtcacat accggaaatc aacgactacc acttcattag catcgctgg 780
900

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ccacttta 1628

<210> 18
<211> 542
<212> PRT
<213> D. melanogaster

<400> 18

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Gly Ala Glu Glu Glu Ala Glu Phe Glu Arg Leu Tyr Ala Ala Pro Ala
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Glu Ile Val Ala Leu Leu Ser Ile Phe Tyr Gly Gly Ile Ser Ile Val
35 40 45

Ala Val Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg
50 . . 55 60

Gln Met Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala
65 . . 70 75 80

Asp Val Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala
85 . . 90 95

Leu Leu Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro
100 105 110

Phe Val Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala
115 120 125

Ile Ala Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg
130 135 140

Pro Thr Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu
145 150 155 160

Ala Leu Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu
165 170 175

Leu Thr Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg
180 185 190

Pro Phe Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe
195 200 205

Arg Tyr Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile
210 215 220

Ser Phe Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala
225 230 235 240

Pro Gly Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys
245 250 255

Lys Lys Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu
260 265 270

Cys Trp Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro
275 280 285

Glu Ile Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp
290 295 300

Trp Leu Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile
305 310 315 320

Tyr Asn Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys
325 330 335

Phe Cys Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser
340 345 350

Met His Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser
355 360 365

Met Arg Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn
370 375 380

Asn Gly Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala
385 390 395 400

Asn Ser Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Asn Val Asn
405 410 415

Gly Gln His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro
420 425 430

Gly Val Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg
435 440 445

Asn Asn Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp
450 455 460

Val Ala Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu
465 470 475 480

Ala Ser Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser
485 490 495

Ser Cys Ile Cys Glu Gln Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly
500 505 510

Thr Cys Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln
515 520 525

Ala Lys Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu
530 535 540

<210> 19
 <211> 1451
 <212> DNA
 <213> D. melanogaster

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aaccatagat ggatttagtgg tagttccaca attcagccag aggagtccct ttatggcact	180
gatttgccca cctatcaaca ttgcataagcc acgcggaaatt ccttgctga cttgttcact	240
gtgggtgtct acggatttgt gtgcattatc ggattatttg gcaacaccct ggtgatctac	300
gtgggtgtgc gctttccaa aatgcaaacg gtcacgaata tatatatcct gaatctggcg	360
gtggcagacg agtgcttcct gatttgaata cccttctgc tgtacacaat gcgaatttgc	420
agctggcgat tcggggagtt tatgtcaaa gcctacatgg tgagcacatc catcacctcc	480
ttcacctcgt cgattttct gctcatcatg tccgcggatc gatataatgc ggtatgccac	540
ccgatttcct cgccacgata tcgaactctg catattgcca aagtggtctc agcgattgcc	600
tggtcaactt cagcggtcct catgctgccc gtgatcctt atgccagcac tgtggagcag	660
gaggatggca tcaattactc gtgcaacata atgtggccag atgcgtacaa gaagcattcg	720
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ctgagttct actacttggt tataaggaaa ctgcgatcgg tgggtcccaa accaggaacg	840
aagtccaagg agaagaggcg ggctcacagg aaggtcactc gactggtaact gacggtgata	900
agtgtataca ttctatgttgc gctccctcac tggatttctc aggtggccct gattcactcg	960
aatccccgcgc aaagggacct ctcccgactg gaaatactca ttttcctact tctggggca	1020
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cagctggagc ccagtgtttt caccaaacag ggcagtaaaa agaggggtgg ctccaagcgc	1200
ctgttgacca gcaatccgca gattcctcca ctgctgccac tgaatgcggg taacaacaat	1260
tcatcgacca ccacatcctc gaccacgaca gcggaaaaga ccggaaccac ggggacacag	1320
aaatcatgca attccaatgg caaagtgaca gctccgccgg agaatttgat tatatgtttg	1380
agcgagcagc aggaggcatt ttgcaccacc gcgagaagag gatcgggcgc agtgcagcag	1440
acagatttgt a	1451

<210> 20
<211> 483
<212> PRT
<213> D. melanogaster

<400> 20

Met Phe Thr Trp Leu Met Met Asp Val Leu Gln Phe Val Lys Gly Glu
1 5 10 15 .

Met Thr Ala Asp Ser Glu Ala Asn Ala Thr Asn Trp Tyr Asn Thr Asn
20 25 30

Glu Ser Leu Tyr Thr Thr Glu Leu Asn His Arg Trp Ile Ser Gly Ser
35 40 45

Ser Thr Ile Gln Pro Glu Glu Ser Leu Tyr Gly Thr Asp Leu Pro Thr
50 55 60

Tyr Gln His Cys Ile Ala Thr Arg Asn Ser Phe Ala Asp Leu Phe Thr
65 70 75 80

Val Val Leu Tyr Gly Phe Val Cys Ile Ile Gly Leu Phe Gly Asn Thr
85 90 95

Leu Val Ile Tyr Val Val Leu Arg Phe Ser Lys Met Gln Thr Val Thr
100 105 110

Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile
115 120 125

Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe
130 135 140

Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser
145 150 155 160

Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile
165 170 175

Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile
180 185 190

Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met
195 200 205

Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile
210 215 220

Asn Tyr Ser Cys Asn Ile Met Trp Pro Asp Ala Tyr Lys Lys His Ser
225 230 235 240

Gly Thr Thr Phe Ile Leu Tyr Thr Phe Phe Leu Gly Phe Ala Thr Pro
245 250 255

Leu Cys Phe Ile Leu Ser Phe Tyr Tyr Leu Val Ile Arg Lys Leu Arg
260 265 270

Ser Val Gly Pro Lys Pro Gly Thr Lys Ser Lys Glu Lys Arg Arg Ala
275 280 285

His Arg Lys Val Thr Arg Leu Val Leu Thr Val Ile Ser Val Tyr Ile
290 295 300

Leu Cys Trp Leu Pro His Trp Ile Ser Gln Val Ala Leu Ile His Ser
305 310 315 320

Asn Pro Ala Gln Arg Asp Leu Ser Arg Leu Glu Ile Leu Ile Phe Leu
325 330 335

Leu Leu Gly Ala Leu Val Tyr Ser Asn Ser Ala Val Asn Pro Ile Leu
340 345 350

Tyr Ala Phe Leu Ser Glu Asn Phe Arg Lys Ser Phe Phe Lys Ala Phe
355 360 365

Thr Cys Met Asn Lys Gln Asp Ile Asn Ala Gln Leu Gln Leu Glu Pro
370 375 380

Ser Val Phe Thr Lys Gln Gly Ser Lys Lys Arg Gly Gly Ser Lys Arg
385 390 395 400

Leu Leu Thr Ser Asn Pro Gln Ile Pro Pro Leu Leu Pro Leu Asn Ala
405 410 415

Gly Asn Asn Asn Ser Ser Thr Thr Ser Ser Thr Thr Ala Glu
420 425 430

Lys Thr Gly Thr Thr Gly Thr Gln Lys Ser Cys Asn Ser Asn Gly Lys
435 440 445

Val Thr Ala Pro Pro Glu Asn Leu Ile Ile Cys Leu Ser Glu Gln Gln
450 455 460

Glu Ala Phe Cys Thr Thr Ala Arg Arg Gly Ser Gly Ala Val Gln Gln
465 470 475 480

Thr Asp Leu

<210> 21
<211> 1754
<212> DNA
<213> D. melanogaster

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aacgtggcac cctacaatgg aactggaaac ggaggcactg tctccttggc gggcaatgcg	180
acaaggcagct atggcgatga tgatagggat ggctatatgg acaccgagcc cagtgacctg	240
gtcaccgaac tggccttctc cctggcacc agttcaagtc caagtcccag ttccacaccc	300
gcttccagct ccagtagttc cactggcatg cccgtctggc tgataccccag ctatagcatg	360
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cggatgcgta ccataaccaa cgtgttcctg ctcaacctgg ccataatcgga catgctgctg	480
ggcgtgctct gcatgcccgt caccctggtg ggcaccctgc tgcgaaactt catcttggc	540
gagttcctct gcaagcttt tcagttctcg caagccgcct ccgtggccgt ttcgtcctgg	600
accttggtgg ccataatcctg tgagcgctac tacgcgatat gccatccact gcgctcgca	660
tcctggcaga caatcagtca cgccatacaag atcatggct tcatctggct gggcggcattc	720
ctctgcatacg cggccatagc ggtcttttagt caattgatac ccaccagtcg accgggctac	780
tgcaagtgcc gtgagtttg gcccgaccag ggatacgagc tcttctacaa catcctgctg	840
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cgtaccctgt acgtaggcat ggccaaggac agcggacgca tcctgcagca atcgctgcct	960
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tgcatcctgg	tcctgaccgc	caccgcagtc	tataatgaaa	atagtaacaa	taataatgga	1080
aattcagagg	gatccgcagg	cggaggatca	accaatatgg	caacgaccac	cttgacaacg	1140
agaccaacgg	ctccaactgt	gatcaccacc	accacgacga	ccacggtgac	gctggccaag	1200
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tacgagtagt	tcgactacac	ggccatcagt	ttcctccagc	tgctggccta	ctcatccagc	1440
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accttcaagg	gtctgccctg	gcgtcgtgga	gcaggtgcc	gcggaggcgt	cggtgtgct	1560
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aacaccaaca	ttagtctcaa	tccggccta	gccatggta	tgggcacctg	gcggagtcgc	1680
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<210> 22
 <211> 584
 <212> PRT
 <213> D. melanogaster

<400> 22

Met	Phe	Asn	Tyr	Glu	Glu	Gly	Asp	Ala	Asp	Gln	Ala	Ala	Met	Ala	Ala
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Ala	Ala	Ala	Tyr	Arg	Ala	Leu	Leu	Asp	Tyr	Tyr	Ala	Asn	Ala	Pro	Ser
					20			25				30			

Ala	Ala	Gly	His	Ile	Val	Ser	Leu	Asn	Val	Ala	Pro	Tyr	Asn	Gly	Thr
				35			40				45				

Gly	Asn	Gly	Gly	Thr	Val	Ser	Leu	Ala	Gly	Asn	Ala	Thr	Ser	Ser	Tyr
	50				55				60						

Gly	Asp	Asp	Asp	Arg	Asp	Gly	Tyr	Met	Asp	Thr	Glu	Pro	Ser	Asp	Leu
	65				70			75			80				

Val	Thr	Glu	Leu	Ala	Phe	Ser	Leu	Gly	Thr	Ser	Ser	Ser	Pro	Ser	Pro
					85			90					95		

Ser Ser Thr Pro Ala Ser Ser Ser Ser Thr Ser Thr Gly Met Pro Val
100 105 110

Trp Leu Ile Pro Ser Tyr Ser Met Ile Leu Leu Phe Ala Val Leu Gly
115 120 125

Asn Leu Leu Val Ile Ser Thr Leu Val Gln Asn Arg Arg Met Arg Thr
130 135 140

Ile Thr Asn Val Phe Leu Leu Asn Leu Ala Ile Ser Asp Met Leu Leu
145 150 155 160

Gly Val Leu Cys Met Pro Val Thr Leu Val Gly Thr Leu Leu Arg Asn
165 170 175

Phe Ile Phe Gly Glu Phe Leu Cys Lys Leu Phe Gln Phe Ser Gln Ala
180 185 190

Ala Ser Val Ala Val Ser Ser Trp Thr Leu Val Ala Ile Ser Cys Glu
195 200 205

Arg Tyr Tyr Ala Ile Cys His Pro Leu Arg Ser Arg Ser Trp Gln Thr
210 215 220

Ile Ser His Ala Tyr Lys Ile Ile Gly Phe Ile Trp Leu Gly Gly Ile
225 230 235 240

Leu Cys Met Thr Pro Ile Ala Val Phe Ser Gln Leu Ile Pro Thr Ser
245 250 255

Arg Pro Gly Tyr Cys Lys Cys Arg Glu Phe Trp Pro Asp Gln Gly Tyr
260 265 270

Glu Leu Phe Tyr Asn Ile Leu Leu Asp Phe Leu Leu Leu Val Leu Pro
275 280 285

Leu Leu Val Leu Cys Val Ala Tyr Ile Leu Ile Thr Arg Thr Leu Tyr
290 295 300

Val Gly Met Ala Lys Asp Ser Gly Arg Ile Leu Gln Gln Ser Leu Pro
305 310 315 320

Val Ser Ala Thr Thr Ala Gly Gly Ser Ala Pro Asn Pro Gly Thr Ser
325 330 335

Ser Ser Ser Asn Cys Ile Leu Val Leu Thr Ala Thr Ala Val Tyr Asn
340 345 350

Glu Asn Ser Asn Asn Asn Gly Asn Ser Glu Gly Ser Ala Gly Gly
355 360 365

Gly Ser Thr Asn Met Ala Thr Thr Thr Leu Thr Thr Arg Pro Thr Ala
370 375 380

Pro Thr Val Ile Thr Thr Thr Thr Thr Val Thr Leu Ala Lys
385 390 395 400

Thr Ser Ser Pro Ser Ile Arg Val His Asp Ala Ala Leu Arg Arg Ser
405 410 415

Asn Glu Ala Lys Thr Leu Glu Ser Lys Lys Arg Val Val Lys Met Leu
420 425 430

Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr Pro Leu Tyr Val
435 440 445

Ile Asn Thr Met Val Met Leu Ile Gly Pro Val Val Tyr Glu Tyr Val
450 455 460

Asp Tyr Thr Ala Ile Ser Phe Leu Gln Leu Leu Ala Tyr Ser Ser Ser
465 470 475 480

Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala Ser Phe Arg Arg
485 490 495

Ala Phe Val Asp Thr Phe Lys Gly Leu Pro Trp Arg Arg Gly Ala Gly
500 505 510

Ala Ser Gly Gly Val Gly Ala Ala Gly Gly Leu Ser Ala Ser
515 520 525

Gln Ala Gly Ala Gly Pro Gly Ala Tyr Ala Ser Ala Asn Thr Asn Ile
530 535 540

Ser Leu Asn Pro Gly Leu Ala Met Gly Met Gly Thr Trp Arg Ser Arg

545	550	555	560			
Ser Arg His Glu Phe Leu Asn Ala Val Val Thr Thr Asn Ser Ala Ala						
565		570	575			
Ala Ala Val Asn Ser Pro Gln Leu						
580						
<210> 23						
<211> 1452						
<212> DNA						
<213> D. melanogaster						
<400> 23						
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gagggtctgg	cactggat	ggccacaat	gccagcgccg	acggcggaa	agtaccgtat	180
tgccccgtgc	tggaccgccc	ggagacgtac	attgtcaccc	tgtgtacac	gctcatcttc	240
attgtggag	ttttggcaa	cggcacgctg	gtcatcatct	tcttcgcca	ccgctccatg	300
cgcaacatac	ccaacacata	cattcttca	ctggccctgg	ctgatctgtt	ggttatattg	360
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ccttcgggttc	ttttctccga	catcaagtcc	taccctgtgt	tcacagccac	cggtaacatg	660
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aaggcactgg	tgtactacct	gttgcgcgtg	tccatcattg	gggcgcata	catcatgtat	780
gccaagcggc	tccatatgag	cgcggcaac	atgcccggcg	aacagcagag	catgcagagc	840
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caaccccg	gcctctactg	cgtgtccggg	gtgtttcg	agcactttaa	tcgctacctc	1080
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aatctgcggg cctcgctgca ccggaacagc aatcacggag ttgggtggagc tggagggtgga 1260
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atgcgctact aa 1452

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<211> 483
<212> PRT
<213> D. melanogaster

<400> 24

Met Tyr Ala Ser Leu Met Asp Val Gly Gln Thr Leu Ala Ala Arg Leu
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Ala Asp Ser Asp Gly Asn Gly Ala Asn Asp Ser Gly Leu Leu Ala Thr
20 25 30

Gly Gln Gly Leu Glu Gln Glu Gln Gly Leu Ala Leu Asp Met Gly
35 40 45

His Asn Ala Ser Ala Asp Gly Gly Ile Val Pro Tyr Val Pro Val Leu
50 55 60

Asp Arg Pro Glu Thr Tyr Ile Val Thr Val Leu Tyr Thr Leu Ile Phe
65 70 75 80

Ile Val Gly Val Leu Gly Asn Gly Thr Leu Val Ile Ile Phe Phe Arg
85 90 95

His Arg Ser Met Arg Asn Ile Pro Asn Thr Tyr Ile Leu Ser Leu Ala
100 105 110

Leu Ala Asp Leu Leu Val Ile Leu Val Cys Val Pro Val Ala Thr Ile
115 120 125

Val Tyr Thr Gln Glu Ser Trp Pro Phe Glu Arg Asn Met Cys Arg Ile
130 135 140

Ser Glu Phe Phe Lys Asp Ile Ser Ile Gly Val Ser Val Phe Thr Leu
145 150 155 160

Thr Ala Leu Ser Gly Glu Arg Tyr Cys Ala Ile Val Asn Pro Leu Arg
165 170 175

Lys Leu Gln Thr Lys Pro Leu Thr Val Phe Thr Ala Val Met Ile Trp
180 185 190

Ile Leu Ala Ile Leu Leu Gly Met Pro Ser Val Leu Phe Ser Asp Ile
195 200 205

Lys Ser Tyr Pro Val Phe Thr Ala Thr Gly Asn Met Thr Ile Glu Val
210 215 220

Cys Ser Pro Phe Arg Asp Pro Glu Tyr Ala Lys Phe Met Val Ala Gly
225 230 235 240

Lys Ala Leu Val Tyr Tyr Leu Leu Pro Leu Ser Ile Ile Gly Ala Leu
245 250 255

Tyr Ile Met Met Ala Lys Arg Leu His Met Ser Ala Arg Asn Met Pro
260 265 270

Gly Glu Gln Gln Ser Met Gln Ser Arg Thr Gln Ala Arg Ala Arg Leu
275 280 285

His Val Ala Arg Met Val Val Ala Phe Val Val Val Phe Phe Ile Cys
290 295 300

Phe Phe Pro Tyr His Val Phe Glu Leu Trp Tyr His Phe Tyr Pro Thr
305 310 315 320

Ala Glu Glu Asp Phe Asp Glu Phe Trp Asn Val Leu Arg Ile Leu Pro
325 330 335

Lys Leu Val Arg Gln Pro Arg Gly Leu Tyr Cys Val Ser Gly Val Phe
340 345 350

Arg Gln His Phe Asn Arg Tyr Leu Cys Cys Ile Cys Val Lys Arg Gln
355 360 365

Pro His Leu Arg Gln His Ser Thr Ala Thr Gly Met Met Asp Asn Thr
370 375 380

Ser Val Met Ser Met Arg Arg Ser Thr Tyr Val Gly Gly Thr Ala Gly
385 390 395 400

Asn Leu Arg Ala Ser Leu His Arg Asn Ser Asn His Gly Val Gly Gly
405 410 415

Ala Gly Gly Gly Val Gly Gly Val Gly Ser Gly Arg Val Gly Ser
420 425 430

Phe His Arg Gln Asp Ser Met Pro Leu Gln His Gly Asn Ala His Gly
435 440 445

Gly Gly Ala Gly Gly Ser Ser Gly Leu Gly Ala Gly Gly Arg Thr
450 455 460

Ala Ala Val Ser Glu Lys Ser Phe Ile Asn Arg Tyr Glu Ser Gly Val
465 470 475 480

Met Arg Tyr

<210> 25
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<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 25

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<210> 26
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 26

Asp Pro Lys Gln Asp Phe Met Arg Phe
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<210> 27

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 27

Pro Asp Asn Phe Met Arg Phe
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 28

Thr Pro Ala Glu Asp Phe Met Arg Phe
1 5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 29

Ser Leu Lys Gln Asp Phe Met His Phe
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 30

Ser Val Lys Gln Asp Phe Met His Phe
1 5

<210> 31
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 31

Ala Ala Met Asp Arg Tyr
1 5

<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 32

Ser Val Gln Asp Asn Phe Met His Phe
1 5

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 33

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe
1 5 10

<210> 34
<211> 10
<212> PRT
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<220>
<223> Novel Sequence

<400> 34

Gly Asp Gly Arg Leu Tyr Ala Phe Gly Leu
1 5 10

<210> 35
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 35

Asp Arg Leu Tyr Ser Phe Gly Leu
1 5

<210> 36

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 36

Ala Pro Ser Gly Ala Gln Arg Leu Tyr Gly Phe Gly Leu
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<210> 37

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 37

Gly Gly Ser Leu Tyr Ser Phe Gly Leu
1 5

<210> 38

<211> 4

<212> PRT

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<223> Novel Sequence

<400> 38

Phe Ile Arg Phe

1

<210> 39

<211> 7

<212> PRT

<213> Artificial Sequence

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<400> 39

Lys Asn Glu Phe Ile Arg Phe
1 5

<210> 40
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 40

Phe Met Arg Phe
1

<210> 41
<211> 7
<212> PRT
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<220>
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<400> 41

Lys Ser Ala Phe Met Arg Phe
1 5

<210> 42
<211> 7
<212> PRT
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<220>
<223> Novel Sequence

<400> 42

Lys Pro Asn Phe Leu Arg Phe
1 5

<210> 43
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 43

Phe Leu Arg Phe
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<210> 44
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 44

Tyr Leu Arg Phe
1

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 45

Lys Pro Asn Phe Leu Arg Tyr
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 46

Thr Asn Arg Asn Phe Leu Arg Phe
1 5

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

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Gly Gln Thr Phe Val Arg Phe
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Lys Ser Val Pro Gly Val Leu Arg Phe
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Trp Ala Asn Gln Val Arg Phe
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Ala Ser Trp Ala Ser Ser Val Arg Phe

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Ala Met Met Arg Phe
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Gly Leu Gly Pro Arg Pro Leu Arg Phe
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Ser Pro Ser Ala Lys Trp Met Arg Phe
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Phe Ile Arg Phe
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Ser Gly Lys Pro Thr Phe Ile Arg Phe
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Ala Glu Gly Leu Ser Ser Pro Leu Ile Arg Phe
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Gly Met Pro Gly Val Leu Arg Phe
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Lys Pro Asn Phe Ile Arg Phe
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Phe Asp Asp Tyr Gly His Leu Arg Phe
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Asp Pro Ala Phe Asn Ser Trp Gly
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<210> 176
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Gly Ser Gly Phe Ser Ser Trp Gly
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Gly Ser Ala Phe Tyr Ser Trp Gly
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Asn Pro Phe His Ser Trp Gly
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<400> 180

Pro Ser Phe His Ser Trp Ser
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Xaa Arg Phe His Ser Trp Gly
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Gln Arg Phe His Ser Trp Gly
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Xaa Val Arg Tyr Arg Gln Cys Tyr Phe Asn Pro Ile Ser Cys Phe
1 5 10 15

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<400> 186

Ala Gln Arg Ser Pro Ser Leu Arg Leu Arg Phe
1 5 10

<210> 187
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<400> 187

Pro Ile Arg Ser Pro Ser Leu Arg Leu Arg Phe
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<210> 189
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<400> 189
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<210> 190
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<212> DNA
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<220>
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<400> 190
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<210> 191
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<220>
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<210> 193
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<210> 195
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<210> 196
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<400> 197
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<210> 198
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<210> 200
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<210> 202
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<210> 203
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<210> 210
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<210> 213
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<210> 214
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<210> 215
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<400> 221
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<210> 222
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<210> 223
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<210> 224

<211> 31
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<400> 224
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<210> 225
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<400> 228
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<220>
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Asp Tyr Gly His Leu Arg Phe
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<210> 231
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<400> 231

Gly Ala Ser Phe Tyr Ser Trp Gly
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<400> 232

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